

Fig. 1a

MET_T9 (SEQ ID NO: 3)

gaattccgcccctcgccgccccgaggcgctttgtgagcagatgcccggagccgag
tggagggcgcgagccagatgccccgacagctgacttgctgagaggaggcggggaggcg
cggagcgcgctgtggtccttgcgcgctgacttctccactgggttcctgggcaccgaaag
ataaacctctcataATGaaggcccccgctgtgcttgcacctggcatcctcgctcctgt
ttaccttgggtgcagaggagcaatggggagtgtaaagaggcactagcaaagtccgagatga
atgtgaatatgaagtatcagcttcccaacttcaccgcggaacacccatccagaatgtca
ttctacatgagcatcacattttccttgggtgccactaactacatttatgttttaaatgagg
aagaccttcagaagggttgctgagtacaagactgggcctgtgctggaacaccagattggt
tcccatgtcaggactgcagcagcaaagccaatttatcaggagggtgtttggaagataaca
tcaacatggctctagtgtgcgacacctactatgatgatcaactcattagctgtggcagcg
tcaacagaggggacctgccagcgacatgtctttccccacaatcatactgctgacatacagt
cggagggttcaactgcatattctccccacagatagaagagcccagccagtgctcctgactgtg
tgggtgagcgccctgggagccaaagtcccttcatctgttaaaggaccgggttcatcaacttct
ttgtaggcaataaccataaattcttcttatttcccagatcatccattgcattcgaatcag
tgagaaggctaaaggaaacgaaagatgggttttatgtttttgacggaccagtcctacattg
atgttttacctgagttcagagattcttacccttaagtatgtccatgcctttgaaagca
acaattttatttacttcttgacgggtccaaagggaactctagatgctcagacttttcaca
caagaataatcagggttctgttccataaactctggattgcattcctacatggaaatgcctc
tggagtgtattctcacagaaaagagaaaaagagatccacaaagaagggaagtgtttaata
tacttcaggctgcgtatgtcagcaagcctggggcccagcttgctagacaaataggagcca
gcctgaatgatgacattcttttcgggggtgttcgcacaaagcaagccagattctgccgaac
caatggatcgatctgccatgtgtgcattccctatcaaataatgtcaacgacttcttcaaca
agatcgctcaacaaaaacaatgtgagatgtctccagcatttttacggaccatcatgagc
actgctttaataggacacttctgagaaattcatcaggctgtgaagcgccgctgatgaat
atcgaacagagtttaccacagctttgcagcgcttgacttattcatgggtcaattcagcg
aagtcctcttaacatctatatccaccttcattaaaggagacctcaccatagctaattcttg
ggacatcagaggggtcgcttcatgcagggttggtgtttctcgatcaggaccatcaaccctc
atgtgaattttctcctggactcccatccagtgctcctcagaagtgttggtggagcatatcat
taaaccaaaatggctacacactgggttatcactgggaagaagatcacgaagatcccattga
atggcttgggctgcagacatttccagtcctgcagtcattgcctctctgccccacccttg
ttcagtggtggctgggtgccacgacaaatgtgtgcgatcggaggaatgcctgagcgggacat
ggactcaacagatctgtctgcctgcaatctacaagggttttcccaaatagtgcacccttg
aaggaggggacaaggctgaccatattgtggctgggactttggatttcggaggaataataaat
ttgatttaaagaaaactagagttctccttggaaaatgagagctgcaccttgactttaagt
agagcacgatgaatacatatgaaatgcacagttgggtcctgccatgaataagcatttcaata
tgtccataattatttcaaattggccacgggacacacaatacagtacatttctcctatgtgg
atcctgtaataacaagtatttgcgcgaaatacgggtcctatggctgggtggcactttactta
ctttaactggaaattacctaaacagtggggaattctagacacatttcaattggtggaaaaa
catgtactttaaaaagtgtgtcaaacagttattcttgaatgttatacccagcccaaacca
tttcaactgagtttgctgttaaattgaaaattgacttagccaaccgagagacaagcatct
tcagttaccgtgaagatcccatgtctatgaaattcatccaaccaaattctttattagt
gtgggagcacaataacagggtgttgggaaaaacctgaattcagttagtgtcccgagaatgg
tcataaatgtgcatgaagcaggaagggaactttacagtggcatgtcaacatcgctctaatt
cagagataatctgttgtaccactccttccctgcaacagctgaatctgcaactccccctga
aaaccaaaagcctttttcatgttagatgggatcctttccaaatactttgatctcatttatg
tacataatcctgtgttttaagccttttgaaaagccagtgatgatctcaatgggcaatgaaa
atgtactggaaattaagggaatgatattgaccctgaagcagttaaagggtgaagtgttaa
aagttggaaataagagctgtgagaatatacacttacattctgaagccgttttatgcacgg
tccccaatgacctgctgaaatgaacagcgagctaaatatagagggtgggattcctgcatt
cctctcatgatgtaataaaggaagccagtgtaattatgttatttctcaggcttaaaaTAAa
tcattaaagctcatttatgtgtgggttttgggtcatcaactc

Fig. 1b

MET T9 (SEQ ID NO: 1)

MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAETPIQNVILHE
HHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFPQDCSSKANLSGGVWKNINM
ALVVDYYDDQLISCGSVNRGTCQRHVFPNHTADIQSEVHCIFSPQIEEPSQCPDCVV
SALGAKVLSSVKDRFINFFVGNTINSSYFPDHPLHSISVRRLKETKDGMFLTDQSYID
VLPEFRDSYPIKYVHAFESNNFIYFLTVQRETLDQTFHTRIIRFCSINSGLHSYMEMP
LECILTEKRKKRSTKKEVFNILQAAYVSKPGAQLARQIGASLNDLILFGVFAQSKPDSA
EPMDRSAMCAFPKIYVNDFFNKIVNKNVRLQHFYGPNEHCNRTLLRNSSGCEARR
DEYRTEFTTALQRVDLFMGQFSEVLLTSISTFIKGLTIANLGTSEGRFMQVVVSRSGP
STPHVNFLLDSDHPVSPEVIVEHTLNQNGYTLVITGKKITKIPLNGLGCRHFQSCSQCLS
APPFVQCGWCHDKCVRSEECLESGTWTQQICLPAIYKVFPNSAPLEGGTRLTICGWDFGF
RRNNKFDLKKTRVLLGNESCTLTLESTMTNLKCTVGPAMNKHFNMSIIISNGHGTTOY
STFSYVDPVITSISPKYGPAGGTLLTLTGNYLNSGNSRHISIGGKTCTLKSVSNSILE
CYTPAQTISTEFAVKLKIDLANRETSIFSREDPIVYEIHPTKSFISGGSTITGVGKNL
NSVSVPRMVINVEAGRNFVACQHRNSSEIICCTTPSLQQLNLQLPLKTKAFFMLDGI
LSKYFDLIYVHNPVFKPFKPVMI SMGNENVLEIKGNDIDPEAVKGEVLKVGKNKSCENI
HLHSEAVLCTVPNDLLKLNSELNIEVGFLHSSHDVNKEASVIMLFSGLK

Fig. 3 (page 1/2)

hsu08818_t9.pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:MET_HUMAN

Sequence documentation:

Hepatocyte growth factor receptor precursor (EC 2.7.1.112) (Met proto- oncogene tyrosine kinase) (c-met) (HGF receptor) (HGF-SF receptor). Homo sapiens (Human). P08581; O60366; Q9UPL8;

Alignment of: HSU08818_T9 x MET_HUMAN ..

```

      1 MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAET 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAET 50

     51 PIQNVILHEHHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFCPCQD 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
     51 PIQNVILHEHHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFCPCQD 100

    101 CSSKANLSGGVWKDNINMALVVDITYDDQLISCGSVNRGTCQRHVFPHNH 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
    101 CSSKANLSGGVWKDNINMALVVDITYDDQLISCGSVNRGTCQRHVFPHNH 150

    151 TADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINFFVGNT 200
      ||||||||||||||||||||||||||||||||||||||||||||||||
    151 TADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINFFVGNT 200

    201 INSSYFPDHPLHSISVRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYV 250
      ||||||||||||||||||||||||||||||||||||||||||||||||
    201 INSSYFPDHPLHSISVRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYV 250

    251 HAFESNNFIYFLTVQRETLDQTFHTRIIRFCSINSGLHSEMPLECIL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||
    251 HAFESNNFIYFLTVQRETLDQTFHTRIIRFCSINSGLHSEMPLECIL 300

    301 TEKRKKRSTKKEVFNILQAAYVSKPGAQLARQIGASLNDDILFGVFAQSK 350
      ||||||||||||||||||||||||||||||||||||||||||||||||
    301 TEKRKKRSTKKEVFNILQAAYVSKPGAQLARQIGASLNDDILFGVFAQSK 350

    351 PDSAEPMDRSAMCAFPKIYVNDFFNKIVNKNVRCLOHFYGPNEHCENR 400
      ||||||||||||||||||||||||||||||||||||||||||||||||
    351 PDSAEPMDRSAMCAFPKIYVNDFFNKIVNKNVRCLOHFYGPNEHCENR 400

    401 TLLRNSSGCEARRDEYRTEFTTALQRVDLFMGQFSEVLLTSISTFIKGD 450
      ||||||||||||||||||||||||||||||||||||||||||||||||
    401 TLLRNSSGCEARRDEYRTEFTTALQRVDLFMGQFSEVLLTSISTFIKGD 450

    451 TIANLGTSEGRFMQVVVSRSRGPSTPHVNFLDSDHPVSPEVIVEHTLNQNG 500
      ||||||||||||||||||||||||||||||||||||||||||||||||
    451 TIANLGTSEGRFMQVVVSRSRGPSTPHVNFLDSDHPVSPEVIVEHTLNQNG 500

    501 YTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCGWCHDKCVRSEE 550
      ||||||||||||||||||||||||||||||||||||||||||||||||
    501 YTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCGWCHDKCVRSEE 550

    551 CLSGTWTQQICLPAIYKVFPNSAPLEGGTRLTICGWDFGFRNNKFDLKK 600
      ||||||||||||||||||||||||||||||||||||||||||||||||
    551 CLSGTWTQQICLPAIYKVFPNSAPLEGGTRLTICGWDFGFRNNKFDLKK 600
```

Fig. 3 (page 2/2)

```
601 TRVLLGNESCTLTLESTMTNLKCTVGPAMNKHFNMSIIISNGHGTQYS 650
    ||||||||||||||||||||||||||||||||||||||||||||
601 TRVLLGNESCTLTLESTMTNLKCTVGPAMNKHFNMSIIISNGHGTQYS 650

651 TFSYVDPVITSISP KYGPMAGGTLLTLTGNYLNSGNSRHISIGGKTCTLK 700
    ||||||||||||||||||||||||||||||||||||||||||||
651 TFSYVDPVITSISP KYGPMAGGTLLTLTGNYLNSGNSRHISIGGKTCTLK 700

701 SVSNSILECYTPAQTI STEFAVKLKIDLANRETSIFS YREDPIVYEIHPT 750
    ||||||||||||||||||||||||||||||||||||||||||||
701 SVSNSILECYTPAQTI STEFAVKLKIDLANRETSIFS YREDPIVYEIHPT 750

751 KSFISGGSTITGVGKNLNSVSVPRMVINVHEAGRNF TVACQHRNSEIIC 800
    ||||||||||||||||||||||||||||||||||||||||||||
751 KSFISGGSTITGVGKNLNSVSVPRMVINVHEAGRNF TVACQHRNSEIIC 800

801 CTTPSLQQLNLQLPLKTKAFFMLDGILSKYFDLIYVHNPVFKPF EKPVMI 850
    ||||||||||||||||||||||||||||||||||||||||||||
801 CTTPSLQQLNLQLPLKTKAFFMLDGILSKYFDLIYVHNPVFKPF EKPVMI 850

851 SMGNENVLEIKGNDIDPEAVKGEVLKVG NKSCENIHLHSEAVLCTVPNDL 900
    ||||||||||||||||||||||||||||||||||||||||||||
851 SMGNENVLEIKGNDIDPEAVKGEVLKVG NKSCENIHLHSEAVLCTVPNDL 900

901 LKLNSELNIEVGFLHSSH D VNKEASVIMLF SGLK 934
    ||||||||
901 LKLNSELNIE..... 910
```

MET structure

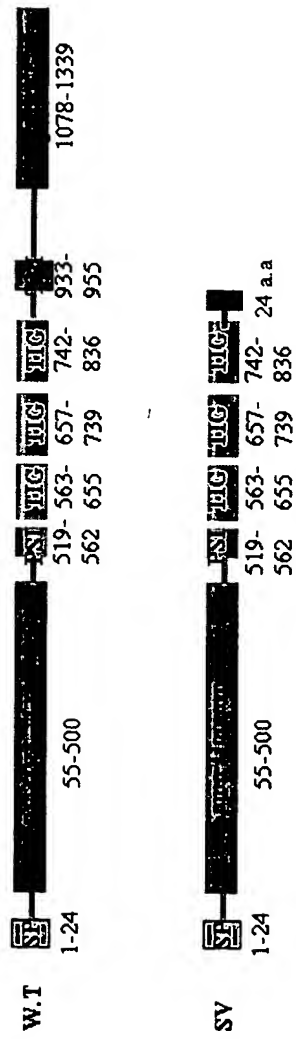


Fig. 4

Fig. 5a

IL6_T6 (SEQ ID NO: 7)

ccatgttttggtaaataagtgttttggtgtgtgcaaggggtctggtttcagcctgaagcca
tctcagagctgtctgggtctctggagactggagggacaacctagtctagagcccatttgc
atgagaccaaggatcctcctgcaagagacaccatcctgaggggaagagggcttctgaacca
gcttgaccaataaagaaattcttgggtgccgacgcggaagcagattcagagcctagagcc
gtgcctgcgtccgtagtttcttctagcttcttttgatttcaaatacaagacttacagggga
gagggagcgataaacacaaaactctgcaagatgccacaagggtcctcctttgacatcccaa
caaagaggactggagatgtctgaggctcattctgcctcgagcccaccgggaacgaaaga
gaagctctatctccccctccaggagcccagctATGaactccttctccacaagcgcttcgg
tccagttgccttctccccctggggctgctcctgggtgtgctgctgccttccctgccccagt
acccccaggagaagattccaaagatgtagccgccccacacagacagccactcacctcttc
agaacgaattgacaaacaaattcggtagacatcctcgacggcatctcagccctgagaaagga
gacatgtaacaagagtaacatgtgtgaaagcagcaaagaggcactggcagaaaacaacct
gaaccttccaaagatggctgaaaaagatggatgcttccaatctggattcaatgaggagac
ttgcctggtgaaaatcatcactgggtcttttgaggtttgaggtatacctagagtacctcca
gaacagatttgagagtagtgaggaacaagccagagctgtgcagatgagtacaaaagtcct
gatccagttcctgcagaaaaaggtgggtgtgtcctcattccctcaacttgggtgtggggga
agacagggtcaaagacagtgtcctggacaactcagggatgcaatgccacttccaaaagag
aaggctacacgtaaacaaaagagctTCAGaaatagtttctgattgttattgttaaattctt
tttttggttggttggttggttggtctcttctgcaaggacatcaa

Fig. 5b

IL-6 T6 (SEQ ID NO: 5)

MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYI
LDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFSQSGFNEETCLVKIITGLL
EFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKVGVSSFPQLGVGEDRLKDSVLDN
SGMQCHFQKRRLHVNKRV

FIGURE 6
Interleukin 6

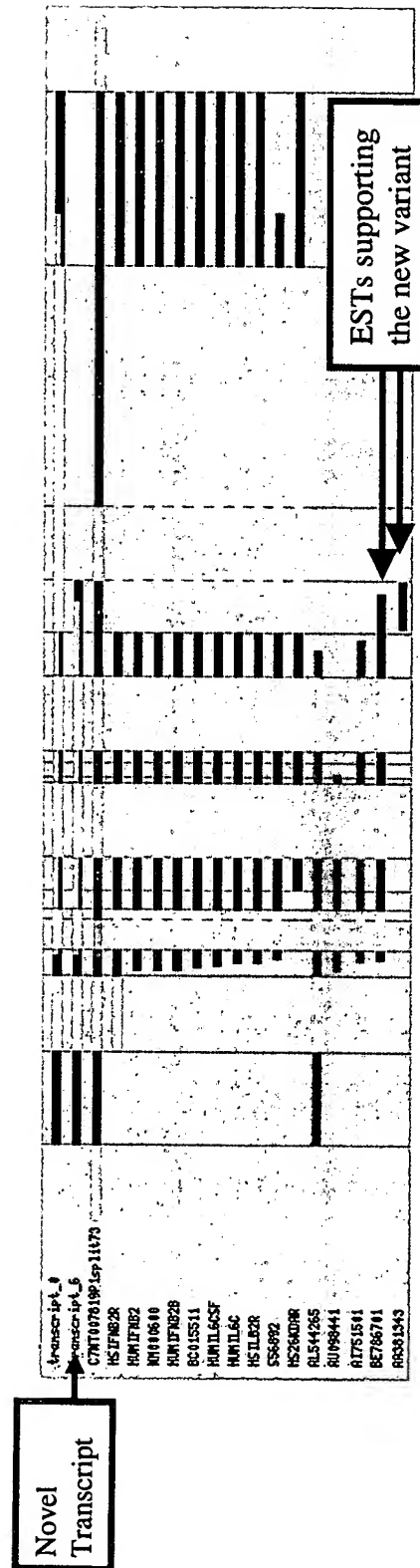


Fig. 7

s56892_p6(t6).pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:IL6_HUMAN

Sequence documentation:

Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2) (Interferon beta-2) (Hybridoma growth factor) (CTL differentiation factor) (CDF). Homo sapiens (Human). P05231; Q9UCU2; Q9UCU3; Q9UCU4;

Alignment of: S56892_P6 x IL6_HUMAN ..

```

      1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS 50
        |||
      1 MNSFSTSAFGPVAFSLGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSS 50

    51 ERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDG 100
        |||
    51 ERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDG 100

   101 CFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVL 150
        |||
   101 CFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVL 150

   151 IQFLQKKVGVSSFPQLGVGEDRLKDSVLDNSGMQCHFQKRRLLHVNKRV 198
        |||
   151 IQFLQKK..... 157
```

IL-6 structure

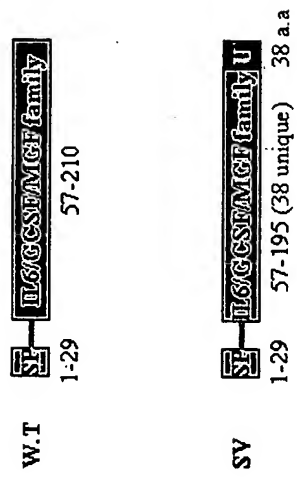


Fig. 8

Fig. 9a

IL-7 T7 (SEQ ID NO: 11)

aagacgaatagtttgatttatttagccaattcagataaatgtgcacgtggaagtcatagtt
aaatattatcgtcagtttccacgtcctgcgtttaatttggggttgattttccaaataca
acacttaccagattaggtggaccacaggattatttttcttgaggtctcacctgagcag
gtgcatgtacagcagacggagcagaaagagactgattagagaggttggagtggtagaggg
cgtgaccctcttaatcattcttccacttcttttttaaagacgacttggcatcgtccacc
acatccgcggcaacgcctccttgggtgtcgtccgcttccaataaaccagcttgcgtcctgc
acacttgtggcttccgtgcacacattaacaactcatgggttctagctcccagtcgccaagc
gttgccaaggcgttgagagatcatctgggaagtcctttaccagaattgctttgattcag
gccagctggtttttctgcggtgattcggaaattcgcgaattcctctggctcctcatccag
gtgcgcgggaagcaggtgcccaggagagaggggataatgaagattccatgctgatgatcc
caaagattgaacctgcagaccaagcgcaaagtagaaactgaaagtacactgctggcggat
cctacggaagttatggaaaaggcaaagcgagagccacgcccgtagtgtgtgcccgcctcc
ttgggatggatgaaactgcagtcgcggcgtgggtaagaggaaccagctgcagagatcacc
ctgcccacacagactcggcaactccgcggaagaccagggtcctgggagtgactatgggc
ggtagagagcttgctcctgctccagttgcggtcatcatgactacgcccgcctcccgcagac
cATGttccatgtttcttttaggtatatctttggacttctctcccctgatccttgttctgtt
gccagtagcatcatctgattgtgatattgaaggtaaagatggcaaacaatatgagagtgt
tctaattggtcagcatcgatcaattattggacagcatgaaagaaattggtagcaattgcct
gaataatgaatttaacttttttaaagacatatctgtgatgctaataaggaaggatgtt
tttattccgtgctgctcgcaagttgaggcaatttcttaaaatgaatagcactgggtgattt
tgatctccacttattaaaagtttcagaaggcacaacaatactgttgaactgcactggcca
ggttaaaggaagaaaaccagctgccctgggtgaagcccaaccaacaaagagtttgtctc
aggactacagaagcagttcacattttacagatcaaacggacgacacacacattctttcca
ctgcaaattgtcctttctccacTAAagggtatcagtttctccaaataaattgtatcaact
tgagggcagacacttaattacatcttattatctcgatccccatcattgcatatccagaaa
gagcacataaagcgtttttcaatgcttatttttagttgatggactatttgtttctttgttt
tgaccaataagactgaataaagataactgaggggaaaaaaattaacaactaatcaggaaa
taaacttttttcggatttatgaaataatttgttgacatgctctacaggagtgccttaac
atacctaattggtaactaaaactgttctctttaattacaaaattcccagcatctatcctac
tatgatactatctgaagataggcaccaataatacaaatgtttatccaaa

Fig. 9b.

IL-7 T7 (SEQ ID NO: 9)

MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDQKQYESVLMVSIQQLDSMKEIGSNCL
NNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLLKVSEGTTILLNCTGQ
VKGRKPAALGEAQPTKSLSSGLQKQFTFYRSNGRHTHSFHCKLSFLH

Fig. 9c

IL7-T8 (SEQ ID NO: 15)

aagacgaatagtttgatttatttagccaattcagataaatgtgcacgtggaagtcatagtt
aaatattatcgtcagtttccacgtcctgctttaatttggggtttgattttccaaataca
acacttaccagattaggtggacccacaggattatttttcccttgaggtctcacctgagcag
gtgcatgtacagcagacggagcagaaagagactgattagagaggttgagtggttagaggg
cgtgaccctcttaatcattcttcacttccttttttaaagacgacttggcatcgtccacc
acatccgcggaacgcctccttggtgtcgtccgcttccaataaccagcttgcgtcctgc
acacttggtggcttccgtgcacacattaacaactcatggttctagctcccagtcgccaagc
gttgccaaggcgttgagagatcatctgggaagtcttttaccagaattgctttgattcag
gccagctggtttttcctgcggtgattcggaaattcgcgaattcctctggctcctcatccag
gtgcgcggaagcaggtgccaggagagaggggataatgaagattccatgctgatgatcc
caaagattgaacctgcagaccaagcgcaaagtagaaaactgaaagtacactgctggcggat
cctacggaagttatggaaaaggcaaagcgagagccacgccgtagtgtgtgccgcccccc
ttgggatggatgaaactgcagtcgcggcgtgggtaagaggaaccagctgcagagatcacc
ctgcccacacagactcggcaactccgcggaagaccagggctcctgggagtgactatgggc
ggtgagagcttgctcctgctccagttgcggtcatcatgactacgcccgcctcccgcagac
cATGttccatgtttcttttaggtatatctttggacttcctcccctgatccttggtctgtt
gccagtagcatcatctgattgtgatattgaaggtaaagatggcaaacaatatgagagtg
tctaattggtcagcatcgatcaattattggacagcatgaaagaaattggtagcaattgcct
gaataatgaatttaacttttttaaagacatatctgtgatgctaataaggaaggtatggt
tttattccgtgctgctcgcaagttgaggcaatttcttaaaatgaatagcactgggtgattt
tgatctccacttattaaaagtttcagaaggcacaacaatactgttgaactgcactggcca
ggttaaaggaagaaaaccagctgccctgggtgaagcccaaccaacaaagagtttgggtgga
actgatcattccttcatgtatgcctccactgctcagctcaacaagtaactctTAAtaacc
taccacctgttatctctgggagagggacatatgtttgccaatttctatcttcaatgctta
tcacaaattttcttatatttgaaataatctgattcaaatgagaactttaacctaaaactt
taattggaaagacaatcttataaaaaatcttataacatattc

Fig. 9d

IL7 T8 (SEQ ID NO: 13)

MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDQYESVLMVSIQQLDSMKEIGSNCL
NNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDFDLHLLKVSEGTTILLNCTGQ
VKGRKPAALGEAQPTKSLVELIIPSCMPPLLSSTSNS

Interleukin 7

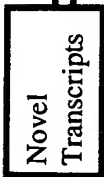


Fig. 11a

humil7a_p4(t7).pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:IL7_HUMAN

Sequence documentation:

Interleukin-7 precursor (IL-7). Homo sapiens (Human). P13232;

Alignment of: HUMIL7A_P4 x IL7_HUMAN ..

```

      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGGKQYESVLMVSIQQLD 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGGKQYESVLMVSIQQLD 50

      51 SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDF 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDF 100

      101 DLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSLSSGLQKQFTFYR 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
      101 DLHLLKVSEGTTILLNCTGQVKGRKPAALGEAQPTKSL..... 138

      151 SNGRHTHSFHCKLSFLH 167

      138 ..... 138
```

Fig. 11b

humil7a_p5 (t8).pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:IL7_HUMAN

Sequence documentation:

Interleukin-7 precursor (IL-7). Homo sapiens (Human). P13232;

Alignment of: HUMIL7A_P5 x IL7_HUMAN ..

```

      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGGKQYESVLMVSIQQLD 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MFHVSFRYIFGLPPLILVLLPVASSDCDIEGKDGGKQYESVLMVSIQQLD 50

      51 SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDF 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 SMKEIGSNCLNNEFNFFKRHICDANKEGMFLFRAARKLRQFLKMNSTGDF 100

      101 DLHLLKVSEGT TILLNCTGQVKGRKPAALGEAQPTKSLVELIIPSCMPPL 150
      ||||||||||||||||||||||||||||||||||||||||||||
      101 DLHLLKVSEGT TILLNCTGQVKGRKPAALGEAQPTKSL..... 138

      151 LSSTSNS 157

      138 ..... 138
```

IL-7 structure



Fig. 12

Fig. 13a

TNFR9 T4 (SEQ ID NO: 19)

gagaccaaggagtggaagttctccggcagccctgagatctcaagagtga
catttgtagaccagctaatttgattaaaattctcttggaatcagctttgctagtatcat
acctgtgccagatttcattcATCgggaaacagctgttacaacatagtagccactctgttgct
ggctcctcaactttgagaggacaagatcattgcaggatccttgtagtaactgccagctgg
tacattctgtgataataacaggaatcagatttgagtcctgtcctccaaatagtttctc
cagcgcagggtggacaaaggacctgtgacatatgcaggcagtgtaaagggtgttttcaggac
caggaaggagtggttcctccaccagcaatgcagagtggtgactgcactccagggtttcactg
cctggggggcaggatgcagcatgtgtgaacaggattgtaaacaaggccaagaactgacaaa
aaaagggtgtaaagactgttgctttgggacatttaacgatcagaaacgtggcatctgtcg
accctggacaaacatcagagtggtgacgaatggaatcatgattcacaagaaaagtatTC
Actattttctcggacttagctgaattctgtctttggaaagtggcttttttaaaaagctgt
tctttggatggaaagtctgtgcttgtgaatgggacgaaggagaggacgtggtctgtgga
ccatctccagccgacctctctccgggagcatcctctgtgaccccgctgcccctgcgaga
gagccaggacactctccgcagatcatctccttcttcttgcgctgacgtcgactgcgttg
ctcttctgctgttcttctcacgctccggttctctgttggttaaaccggggcagaaagaaa
ctcctgtatatattcaacaacgtaagattaacataatcatattacagctctggca

Fig. 13b

TNFR9 T4 (SEQ ID NO: 17)

MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQR
TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCKDC
CFGTFNDQKRGICRPWTNIRVADEWNHDSQEKY

FIGURE 14
Tumor necrosis factor receptor-9/4-1BB

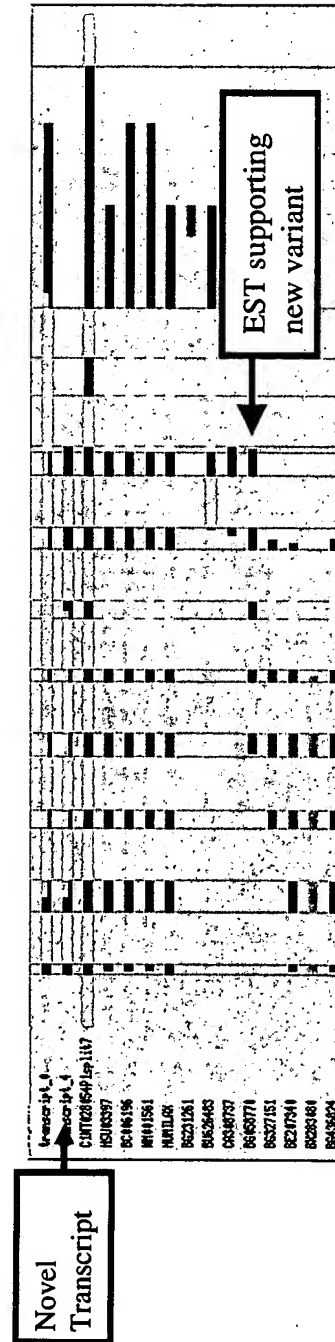


Fig. 15

hsu03397_p4 (T4).pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:TNR9_HUMAN

Sequence documentation:

Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA) (CD137 antigen). Homo sapiens (Human). Q07011;

Alignment of: HSU03397_P4 x TNR9_HUMAN ..

```

      1 MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPP 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPP 50

      51 NSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCS 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 NSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCS 100

      101 MCEQDCKQGQELTKKGCKDCCFGTFNDQKRGICRPWTNIRVADEWNHDSQ 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
      101 MCEQDCKQGQELTKKGCKDCCFGTFNDQKRGICRPWTN..... 138

      151 EKY 153

      138 ... 138
```

TNFR 9- structure

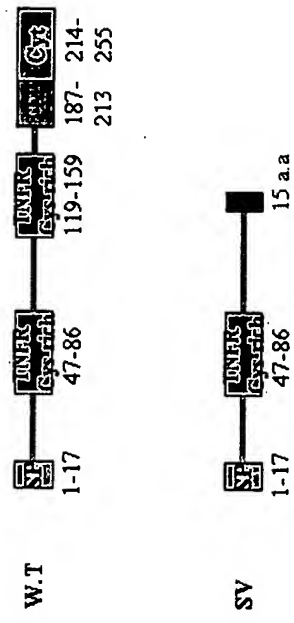


Fig. 16

Fig. 17b

IL-4R T4 (SEQ ID NO: 21)

MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKQNGPTNCSTELR
LLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS
EHVLPPLKRSWSQ

Fig. 17c

IL-4R T11 (SEQ ID NO: 27)

tgcaagtccccgacagattgtactagttactgattgaagggctgttttactatccaaatgtggctggagtaggagttgggt
aaacattttattgaagaatgtgcaaccactctcacttggagccgggctgttaggaaggggaggaggattccagtcgcca
gccctccccaccaaactgccccggcgcaaaagaggccgaggagccaggcaggagcaggtcctggaggcctggt
cggcgtgggctgtttattccgagaccaaggggatccactgcagagttctccgctgggctgacctcgggctacggcgtgg
gaggaagcgcgcggcaagacacccagcgaggtgctggggctcggggcaggagagcggcggctcggactgtccggcggc
ggcggcggggacagcgacaggggcgaggtggcgggacccgggcccggcgcgccgggcccgggcccggcgcatgcaaatct
gccccgcgcggggcgaggagcaggaagccggggcgggctgggtctccgcgccaggaaagccccgcgcggcgcgggcca
gggaagggccacccagggtccccacttcccgcttggcgcccggagcggcgaatggagcagggcgcgagataattaa
agatttacacacagctggaagaaatcatagagaagccggcggtgggtcctatgcctataatcccagcacttttgaggc
tgaggcgggcagatcacttgagatcaggagttcgagaccagcctggtgccttggcatctcccaATGgggtggcttggctc
tgggctcctgttccctgtgagctgctgggtcctgctgcaggtggcagctctgggaacatgaaggtccttgaggagccca
cctgctctccgactacatgagcatctctacttgcgagtggaagatgaatgggtcccaccaattgcagcaccgagctccgc
ctgttgtagcagctggtttttctgctctccgaagccacacgtgtatccctgagaacaacggaggcgcggggtgctgtg
ccacctgctcatggatgacgtggtcagtgcgataactatacactggacctgtgggctgggcagcagctgctgtggaagg
gctccttcaagcccagcgagcatgtgaaacccagggccccaggaacctgacagttcacaccaatgtctccgacactctg
ctgctgacctggagcaacccgtatccccctgacaattacctgtataatcatctcacctatgcagtcaacatttgagtg
aaacgacccggcagatttcagaatctataacgtgacctacctagaacctccctccgcatcgagccagcaccctgaagt
ctgggatttctacagggcacgggtgagggcctgggctcagtgctataacaccacctggagtgagtgaggccccagcacc
aagtggcacaactgtgagtatcaagaggccTAAgcaatggtaatctccactctccattcttccccctgtggccagacactt
ccccctggctgagtcctctgggc

Fig. 18

IL-4R T11 (SEQ ID NO: 25)

MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMGPTNCSTELR
LLYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLWKGSFKPS
EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPDPNYLYNHLTYAVNIWSENDPADFRIYNV
TYLEPSLRIAASTLKSGISYRARVRAWAQCYNNTWSEWSPSTKWHNCEYQEA

FIGURE 2
Met- Hepatocyte growth factor receptor-

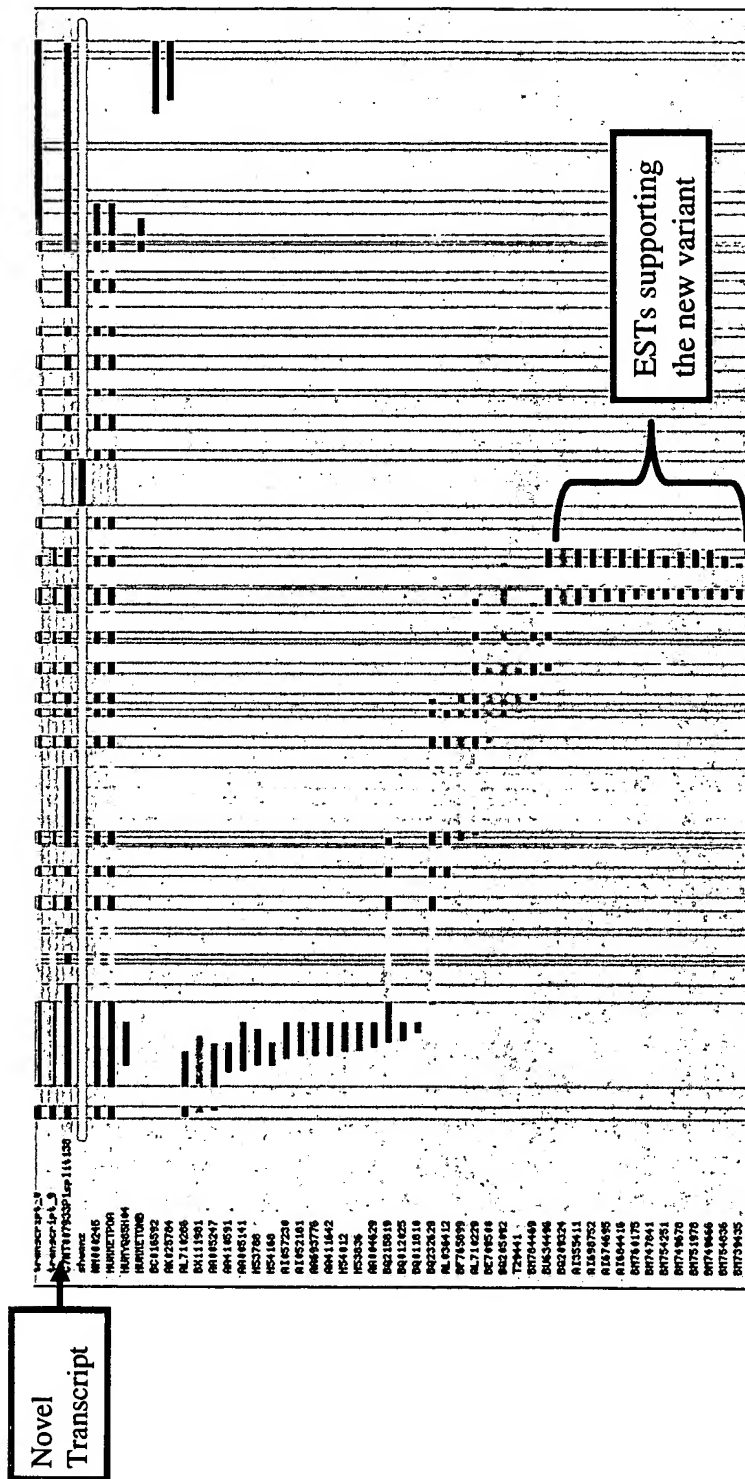


Fig. 19a

cds-2_hsil4r_t4.pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:IL4R_HUMAN

Sequence documentation:

Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen). Homo sapiens (Human). P24394; Q96P01;

Alignment of: CDS-2_HSIL4R_T4 x IL4R_HUMAN ..

```

      1 MGWLC SGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMN 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MGWLC SGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMN 50

      51 PTNCSTELRLLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYT 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 PTNCSTELRLLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYT 100

      101 LDLWAGQQLLWKGSFKPSEHVL PPLKRSWSQ                      131
           ||||||||||||||||||||
      101 LDLWAGQQLLWKGSFKPSEHV.....                          121
```

Fig. 19b

cds-2_hsil4r_t11.pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:IL4R_HUMAN

Sequence documentation:

Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen). Homo sapiens (Human). P24394; Q96P01;

Alignment of: CDS-2_HSIL4R_T11 x IL4R_HUMAN ..

```

      1 MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMN 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MGWLCSGLLFPVSCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMN 50

      51 PTNCSTELRLLYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVSADNYT 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
      51 PTNCSTELRLLYQLVFLLEAHTCIPENNGGAGCVCHLLMDDVVSADNYT 100

      101 LDLWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLTLLTWSNPYPPD 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
      101 LDLWAGQQLLWKGSFKPSEHVKPRAPGNLTVHTNVSDTLTLLTWSNPYPPD 150

      151 NYLYNHLTYAVNIWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRAR 200
      ||||||||||||||||||||||||||||||||||||||||||||||||
      151 NYLYNHLTYAVNIWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRAR 200

      201 VRAWAQCYNNTTSEWSPSTKWHNCEYQEA 229
      ||||||||||||||||||||
      201 VRAWAQCYNNTTSEWSPSTKWHN..... 223
```

IL4R structure



Fig. 20

Fig. 21a

TGR2_T7 (SEQ ID NO: 31)

acctaaagaaaaacatttttacaacttgacagtgtatgcacatacatatgcatatagac
acaactgaagcacaattttaatgaagtagaattttaccgttactatttttatttgggaaaga
aatgtgctcgcgactcaatagattggagatttctactcctggatctcaacttgcaatttga
aaacgcattctctaaagcacctaggagcaatctgaagaaagctgaggggagggcggcagatg
ttctgatctactagggaaaacgtggacgttttctgttggttactttgtgaactgtgtgcac
ttagtcattctttagtaataacttggagcgaggaactcctgagtgggtgtgggagggcgggt
gaggggagcagctgaaagtcggccaaagctctcggaggggctgggtctaggaaacatgattgg
cagctacgagagagctaggggctggacgtcgaggagagggagaaggctctcgggaggaga
gaggtcctgccagctgttggcgaggagtttctgtttccccgcagcgtgagttgaag
ttgagtgaagtactcgcgcgcacggagcgacacacccccgcgcgtgcacccgctcggga
caggagccggactcctgtgcagcttccctcggccgcgggggctccccgcgcctcgcgcg
gcctccaggccccctcctggctggcgagcggggcgccacatctggcccgcacatctgcgct
gccggcccggcgcgggggtccggagagggcgcgccgagggcgagccaggggtccggga
aggcgccgtccgctgcgctgggggctcgggtctatgacgagcagcgggggtctgccATCgggt
cgggggctgtcaggggctgtggccgctgcacatcgctcctgtggacgcgtatcgccagc
acgatcccaccgcagcttcagaagtcgggttaataacgacatgatagtcactgacaacaac
gggtgcagtcaagtttccacaactgtgttaattttgtgatgtgagattttccacctgtgac
aaccagaaatcctgcatgagcaactgcagcatcacctccatctgtgagaagccacaggaa
gtctgtgtggctgtatggagaaagaatgacgagaacataaacactagagacagtttgccat
gacccaagctccccaccatgactttattctggaagatgctgcttctccaaagtgcatt
atgaaggaaaaaaaagcctgggtgagactttcttcatgtgttctctgtagctctgatgag
tgcaatgacaacatcatcttctcagaagggtgagttttcttctcttaagggtgtgggacct
gagatctgtgccaattttttgtatccttgggtctgcagtgctcaTACagcacattcctcctg
tggtggattgcatacagtgagtaggagctcattcagctgggtggaaagaggggcttgggg
agtagcaggggttgttctggttctcatcaaatatgggtgactggggcaaacattattatt
tgtctttgacaaatagtttctttcacctagagcagtggttctcaaagtgcggcccccttga
gcagccagcatcagtatcacctgggaacctgttataaatgcagattctcaggccccacta
aatgagaaacatagaggggtgaacccagctatctgtatttttaacaagccctcccagtaat
tctgtgcagctaaaatttggtaactattgttctaaagatttggatgggggttgtttaatct
tggaggaggactttctttataactgatgttgttcttgtacatagtcccaggatttgtct
ttaggggtacttgtcatcgatcccatttgagagacactttgcaatacagag

Fig. 21b

TGR2_T7 (SEQ ID NO: 29)

MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQLCKFCDVRFST
CDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITLETVCHDPKLPYHDFILEDAAASP
CIMKEKKKPGETFFMCSSDECNDNIIFSEGEFSSLKGVGPEICANFLYPWSAVS

FIGURE 22
Transforming growth factor β receptor type II (TGF- β -R)

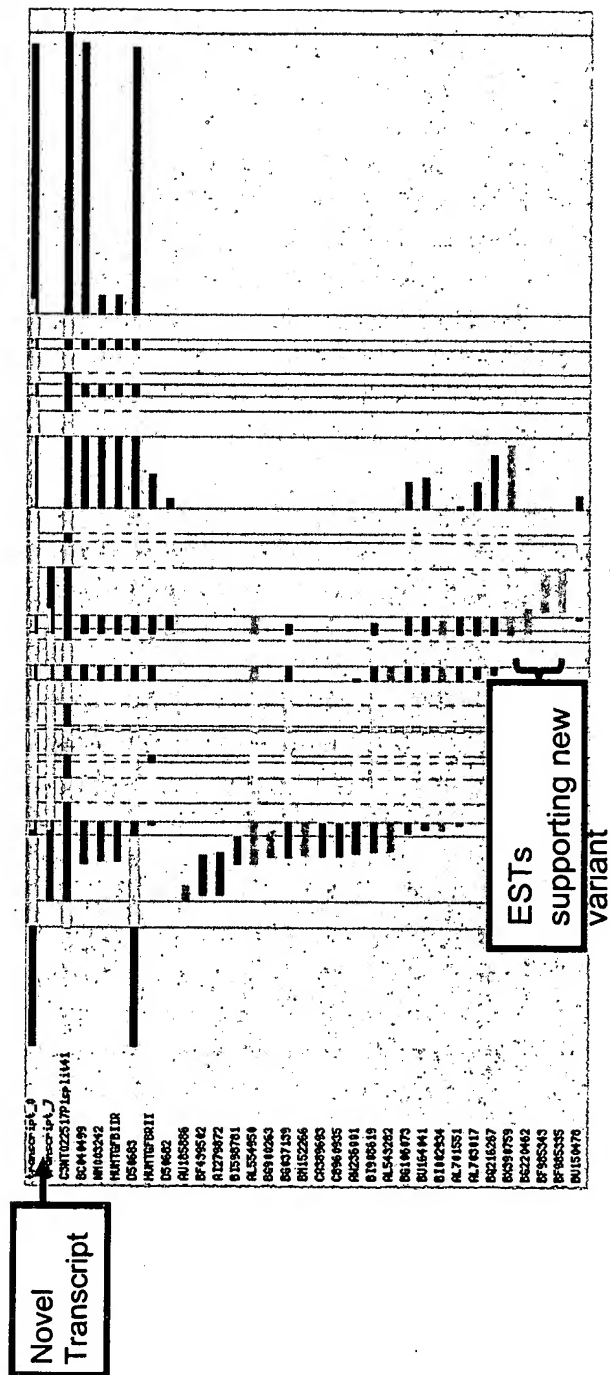


Fig. 23

z21887_p6(t7).pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:TGR2_HUMAN

Sequence documentation:

TGF-beta receptor type II precursor (EC 2.7.1.37) (TGFR-2) (TGF-beta type II receptor). Homo sapiens (Human). P37173; Q99474;

Alignment of: Z21887_P6 x TGR2_HUMAN ..

```

      1 MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQL 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MGRGLLRGLWPLHIVLWTRIASTIPPHVQKSVNNDMIVTDNNGAVKFPQL 50

     51 CKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITLETV 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
     51 CKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITLETV 100

    101 CHDPKLPYHDFILEDAAAPKCIMKEKKKPGETFFMCSCSSDECNDNIIFS 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
    101 CHDPKLPYHDFILEDAAAPKCIMKEKKKPGETFFMCSCSSDECNDNIIFS 150

    151 EGEFSSLKGVGPEICANFLYPWSAVS                               176
      |
    151 E.....                               151
```

TGR2 structure

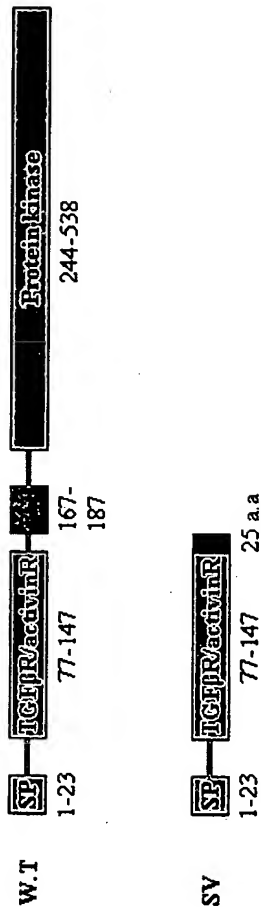


Fig. 24

Fig. 25a

ITAV_T3 (SEQ ID NO: 35)

gataaaaagcttttctcatttttaaaacaacagtcgcacggaagttcccgccgggacaagg
gaacgtgggtgcccttgctactcccgctggacgaggtagattgggacgctggaccgtatc
tccccgccccgcacgcctcctcaggtgctcagcctgaggccttcgtccaggagcg
ctgccgctgacccaggctcaggagctggggggccctgcacagacgcccaggctctcgggac
aggcggcgactgcactcacggaagtacgctgagctctccctgtagaagggcgctctcc
tccccacttctcctccagctccacagcagcctcccgggccggctcctcctcctccag
gtctcctcccagtgccgcccgggctctcaggcctgaggtgcccgcgtcaccccggcagtc
cccagcctcagacgctgctggagcggcgaggcggagggaagcaaaggaccgtctgcgc
tgctgtccccgccccgcgcgtctgcgccccctcgtccctggcggctcgtccgaagctcag
ccctcttgctgccccggagctgtcccgggctagccgagaagagagcggccggcgaagttt
ggcgccgcgcaggcggcgggcgccgcccactggggcgctcgtggggcgggggagggtgg
ctaccgctccccggttgccgctcccgccgcacttcggcgATCgcttttccgcccggcgga
cggctgcccctcgggtccccgcccctcccgcttcttctctcgggactcctgctacctctg
tgccgcgccttcaacctagacgtggacagctcctgcccagtagctctggccccgaggggaagt
tacttcggcttcgcccgtggatttcttcgtgcccagcgcgtcttcccggatgtttctctc
gtgggagctcccaaagcaaaccaccagcctgggattgtggaaggaggcaggtcctc
aaatgtgactggctcttctaccgcccgtgccagccaattgaatttgatgcaacaggcaat
agagattatgccaaggatgatccattggaatttaagtcccatcagtgggttgaggcatct
gtgaggtcgaaacaggataaaaattttggcctgtgccccattgtaccattggagaactgag
atgaaacaggagcgagagcctgttggaacatgctttcttcaagatggaacaaagactgtt
gagtatgctccatgtagatcacaagatattgatgctgatggacagggattttgtcaagga
ggattcagcattgattttactaaagctgacagagtagcttcttggtggctcctggtagcttt
tattggcaaggctcagcttatttcggatcaagtggcagaaatcgtagctctaaatacagcccc
aatgtttacagcatcaagtataataaccaattagcaactcggactgcacaagctattttt
gatgacagctatttgggttattctgtggctgtcggagatttcaatgggtgatggcatagat
gactttgtttcaggagttccaagagcagcaaggactttgggaatgggtttatatttatgat
gggaagaacatgtcctccttatacaattttactggcgagcagatggctgcatatttcgga
ttttctgtagctgccactgacattaatggagatgattatgcagatgtgtttattggagca
cctctcttcatggatcgtggctctgatggcaactccaagagggtggggcaggctctcagtg
tctctacagagagcttcaggagacttcagacgacaaagctgaatggatttgaggtcttt
gcacgggtttggcagtgccatagctcctttgggagatctggaccaggatgggttcaatgat
attgcaattgctgtccatattgggggtgaagataaaaaaggaattgtttatatcttcaat
ggaagatcaacaggcttgaacgcagctcccatctcaaactcctgaagggcagtgggctgct
cgaagcatgccaccaagctttggctatttcaatgaaaggagccacagatatagacaaaaat
ggatatccagacttaattgtaggagcttttgggtgtagatcgagctatcttatacaggggc
agaccagttatcactgtaaatgctggcttctgaagtgtaccctagcattttaaatcaagac
aataaaacctgctcactgcctggaacagctctcaaagtttctgttttaatgttaggttc
tgcttaaaggcagatggcaaaggagtagcttcccaggaaacttaatttccagggtggaactt
cttttgataaaactcaagcaaaaggagcaatttcgacgagcactgtttctctacagcagg
tccccagctcactccaagaacatgactatttcaagggggggactgatgcagtgtagggaa
ttgatagcgtatctgcgggatgaatctgaatttagagacaaactcactccaattactatt
tttatggaatatcggttggttatagaacagctgctgatacaacaggcttgcaaccatt
cttaaccagttcacgcctgctaaccattagtcgacaggctcacattctacttgactgtggt
gaagacaatgtctgtaaacccaagctggaagtttctgtagatagtgatcaaaagaagatc
tatattggggatgacaaccctctgacattgattgttaaggctcagaatcaaggagaaggt
gcctacgaagctgagctcatcggtttccattccactgcaggctgatttcatcggggtgtc
cgaaacaatgaagccttagcaagactttcctgtgcatttaagacagaaaaccaaactcgc
cagggtggtatgtgaccttggaacccaatgaaggctggaactcaactcttagctggtcct
cgtttcagtggtgaccagcagtcagagatggatacttctgtgaaatttgacttacaaatc
caaagctcaaactctatttgacaaagtaagcccagttgtatctcaciaaagttgatcttgct
gttttagctgcagttgagataagaggagctctcgagctcctgatcatatctttctccgatt
ccaaactgggagcacaaggagaaccctgagactgaagaagatgttgggccagttgttcag
cacactctatgaggtttgcagttgtTACattttactcaaacctcgtgagcaagccaacgaa
gagaggaacaactaagctactttaaaaaaaattctatgtaatttttatgtaaaactcta
cattgggttaagtagtgctcagagatttcttgaatattttccctatacataaattcattt
ttatttgacaaatgacttggttaataaagcagtttatataatttggtgtttaaaataa
attagttctacttgaataa

Fig. 25b

ITAV_T3 (SEQ ID NO: 33)

MAFP PRRRLRLGPRGLPLLLSGLLLPLCRAFNLVDSPA EYSGPEG SYFGFAVDFFVPSA
SSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSSTRRCQPIEF DATGNRDYAKDDPLEFKS
HQWFGASVRSKQDKILACAPLYHWRTEMKQEREPVGTCFLQDGT KTVEYAPCRSQDIDAD
GQGFCQGGFSIDFTKADRVLLGGPGSFYWQQLISDQVAEIVSKYDPNVYSIKYNNQLAT
RTAQAI FDDSYLGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE
QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRASGDFQTTK
LNGFEVFARFGSAIAPLGDL DQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQI
LEGQWAARSMPPSFGYSMKGATDIDKNGYPDLIVGAFGVDRAILYRARPVITVNAGLEVY
PSILNQDNKTCSLPGTALKVSCFNVRFLKADGKGVLPRKLN FQVELLLDKLKQKGAI RR
ALFLYSRSPSHSKNMTISRGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAAD
TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVDS DQKKIYIGDDNPLTLIVK
AQNQGE GAYEAELIVSIPLQADFIGVVRNNEALARLSCAFKTENQTRQVCDLGNPMKAG
TQLLAGLRFSVHQQSEMDTSVKFDLQIQSSNLFDKVSPV VSHKVDLAVLA AVEIRGVSSP
DHIFLPIPNWEHKENPETEEDVGPVVQHIYEVCSC

Integrin alpha-V

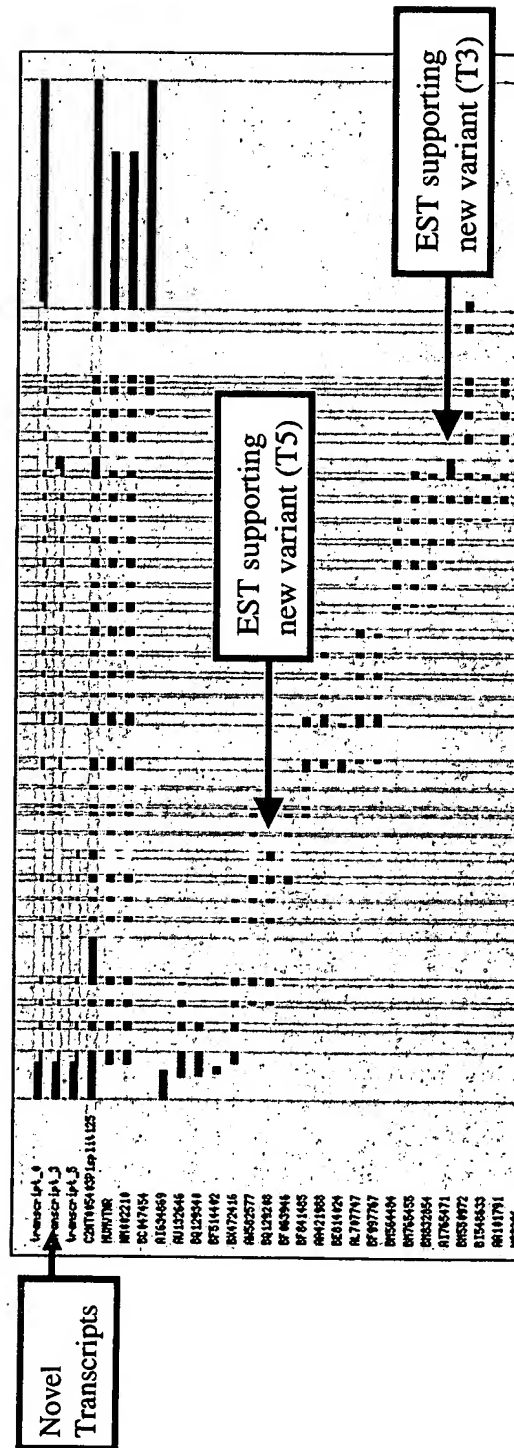


Fig. 27 (page 1/2)

humvtnr_p3(t3).pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:ITAV_HUMAN

Sequence documentation:

Integrin alpha-V precursor (Vitronectin receptor alpha subunit) (CD51 antigen). Homo sapiens (Human). P06756;

Alignment of: HUMVTNR_P3 x ITAV_HUMAN ..

```

      1 MAFPPRRRLRLGPRGLPLLLSGLLLPLCRAFNLVDSPAEGSYFG 50
      ||||||||||||||||||||||||||||||||||||||||
      1 MAFPPRRRLRLGPRGLPLLLSGLLLPLCRAFNLVDSPAEGSYFG 50

     51 FAVDFFVPSASSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPI 100
      ||||||||||||||||||||||||||||||||||||||||
     51 FAVDFFVPSASSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPI 100

    101 EFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQ 150
      ||||||||||||||||||||||||||||||||||||||||
    101 EFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQ 150

    151 EREPVGTCFLQDGTKTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVL 200
      ||||||||||||||||||||||||||||||||||||||||
    151 EREPVGTCFLQDGTKTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVL 200

    201 LGGPGSFYWQQLISDQVAEIVSKYDPNVYSIKYNNQLATRTAQAIFFDD 250
      ||||||||||||||||||||||||||||||||||||||||
    201 LGGPGSFYWQQLISDQVAEIVSKYDPNVYSIKYNNQLATRTAQAIFFDD 250

    251 YLGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE 300
      ||||||||||||||||||||||||||||||||||||||||
    251 YLGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE 300

    301 QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSQGLQEVGQVSVSLQ 350
      ||||||||||||||||||||||||||||||||||||||||
    301 QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSQGLQEVGQVSVSLQ 350

    351 RASGDFQTTKLNGFEVFARFGSAIAPLGDLQDGFNDIAIAAPYGGEDKK 400
      ||||||||||||||||||||||||||||||||||||||||
    351 RASGDFQTTKLNGFEVFARFGSAIAPLGDLQDGFNDIAIAAPYGGEDKK 400

    401 GIVYIFNGRSTGLNAVPSQILEGQWAARSMPPSFGYSMKGATDIDKNGYP 450
      ||||||||||||||||||||||||||||||||||||||||
    401 GIVYIFNGRSTGLNAVPSQILEGQWAARSMPPSFGYSMKGATDIDKNGYP 450

    451 DLIVGAFGVDRAILYRARPVITVNAGLEVYPSILNQDNKTCSLPGTALKV 500
      ||||||||||||||||||||||||||||||||||||||||
    451 DLIVGAFGVDRAILYRARPVITVNAGLEVYPSILNQDNKTCSLPGTALKV 500

    501 SCFNVRFLKADGKGVLPKLNQVVELLLDKLKQKGAIRRALFLYSRSPS 550
      ||||||||||||||||||||||||||||||||||||||||
    501 SCFNVRFLKADGKGVLPKLNQVVELLLDKLKQKGAIRRALFLYSRSPS 550

    551 HSKNMTISRGGMLQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAAD 600
      ||||||||||||||||||||||||||||||||||||||||
    551 HSKNMTISRGGMLQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAAD 600
```

Fig. 27 (page 2/2)

```
601 TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVSDSQKKIYIG 650
    ||||||||||||||||||||||||||||||||||||||||||||||||
601 TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVSDSQKKIYIG 650

651 DDNPLTLIVKAQNQGEGAYEAEIVSIPLQADFIGVVRNNEALARLSCAF 700
    ||||||||||||||||||||||||||||||||||||||||||||||||
651 DDNPLTLIVKAQNQGEGAYEAEIVSIPLQADFIGVVRNNEALARLSCAF 700

701 KTENQTRQVVCDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLQIQSS 750
    ||||||||||||||||||||||||||||||||||||||||||||||||
701 KTENQTRQVVCDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLQIQSS 750

751 NLFDKVSPVVS HKVDLAVLA AVEIRGVSSPDHIFLPIPNWEHKENPETEE 800
    ||||||||||||||||||||||||||||||||||||||||||||||||
751 NLFDKVSPVVS HKVDLAVLA AVEIRGVSSPDHIFLPIPNWEHKENPETEE 800

801 DVGPPVQHIYEVCSC 815
    |||||||||
801 DVGPPVQHIYE.... 811
```

ITAV structure

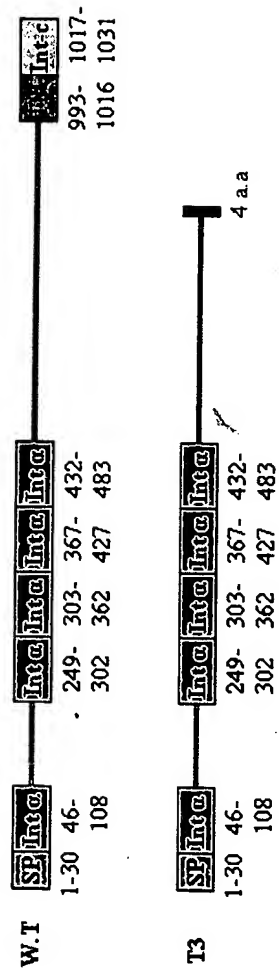


Fig. 28

Fig. 29a

IL-10-R- β _T1 (SEQ ID NO: 39)

ccccccatctccgctgggttcccgaagccgcgcgggacaagctctccggggcgcgggcg
ggggtcgtgtgcttggaggaagccgcggaacccccagcgccggtccATGgcgtggagcct
tgaggagctggctgggtggctgctgctggtgtcagcattgggaatggtaccacctccga
aaatgtcagaatgaattctgttaatttcaagaacattctacagtgggagtcacctgcttt
tgccaaaggggaacctgactttcacagctcagtaacctaatgttataggatattccaagataa
atgcatgaatactaccttgacggaatgtgattttctcaagtctttccaagtatggtgacca
caccttgagagtcagggctgaatttgcagatgagcattcagactgggtaaacatcacctt
ctgtcctgtggatgacaccattattggacccccctggaatgcaagtagaagtaacttgctga
ttctttacatatgcgtttcttagccccctaaaattgagaatgaatacgaacttggtactat
gaagaatgtgtataactcatggacttataatgtgcaatactggaaaaacgggtactgatga
aaagtttcaaattactccccagtatgactttgaggtcctcagaaacctggagccatggac
aacttattgtgttcaagttcgaggggtttcttccctgatcggaacaaagctggggaatggag
tgagcctgtctgtgagcaaacacccatgaCGtttttggggccatcctcatcaTAAacac
ttctgtttttctcctttccattgtcggatgagaatgatgtttttgacaagctaagtgtca
ttgcagaagactctgagagcgggaagcagaatcctggtgacagctgcagcctcgggaccc
cgcttgggcagggggcccccagctaggctctgagaaggaaacacactcggctgggacag
tgacgtactccatctcacatctgcctcagtgagggatcagggcagcaacaaggccaag
accatctgagccagccccacatctagaactccagacctggacttagccaccagagagc
tacattttaaggctgtcttggcaaaaatactccatttgggaactcactgccttataaag
gctttcatgatgttttcagaagttggccactgagagtgtaattttcagccttttatatca
ctaaaataagatcatgttttaattgtgagaaacagggccgagcacagtggctcacgcctg
taataccagcaccttagaggtcgaggcaggcggatcacttgaggtcaggagttcaagacc
agcctggccaatatggtgaaacccagctctctactaaaaatacaaaaattagctaggcatg
atggcgcatgcctataatcccagctactcgagtgcctgaggcaggagaattgcatgaacc
cgggaggaggaggaggaggttgacgtgagccgagatagcggcactgcactccagcctggg
tgacaaagtgagactccatctcaaaaaaaaaaaaaaaaaaattgtgagaaacagaaatact
taaaatgaggaataagaatggagatgttacatctggtagatgtaacattctaccagatta
tggtatggactgatctgaaaatcaacctcaactcaagggtgggtcagctcaatgctacacag
agcacggacttttggattctttgcagtactttgaattttttttctacctatatatgttt
tatatgctgctggtgctccattaaagttttactctgtgttgactatatgtgttcatgat
aaaaaa

Fig. 29b

IL-10-R- β _T1 (SEQ ID NO: 37)

MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYR
IFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDWVNITFCPVDDTIIGPPGMQV
EVLADSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRN
LEPWTTYCVQVRGFLPDRNKAGEWSEPVEQTTHDVFGPSSS

FIGURE 30

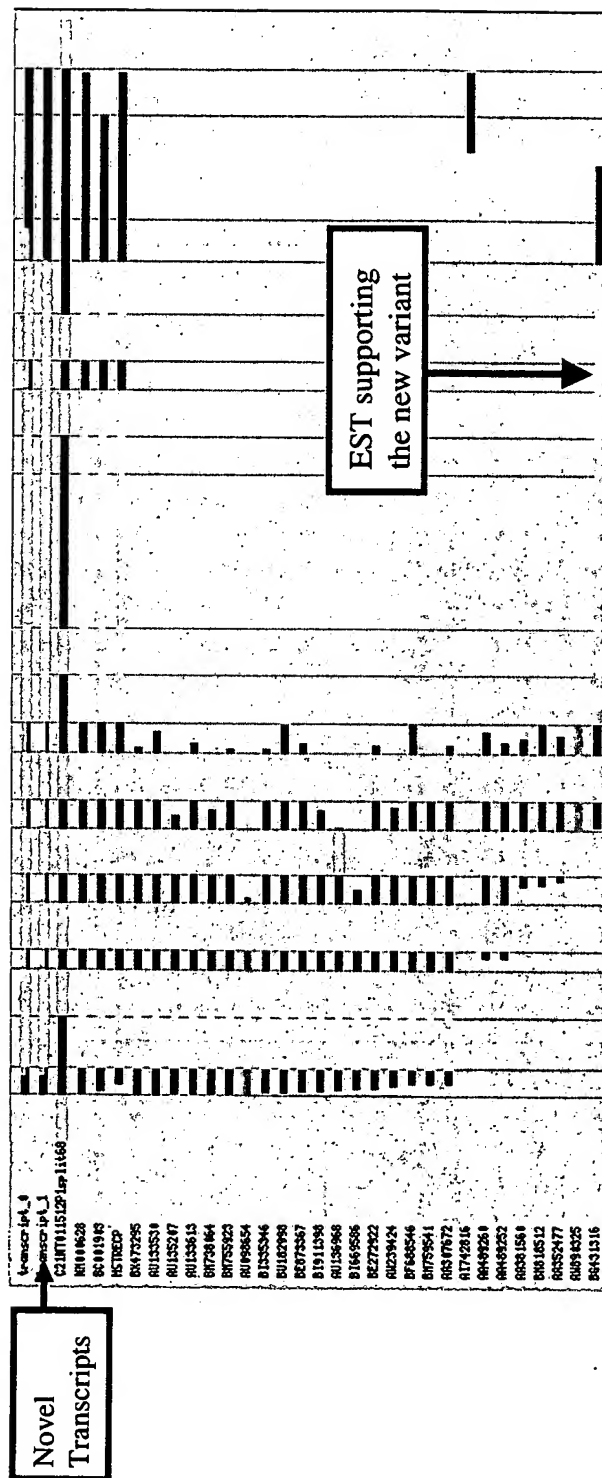


Fig. 31

t48767_p2(t1).pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:I10S_HUMAN

Sequence documentation:

Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
(Cytokine receptor class-II CRF2-4). Homo sapiens (Human). Q08334;

Alignment of: T48767_P2 x I10S_HUMAN ..

```

      1 MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNL 50
      ||||||||||||||||||||||||||||||||||||||||||||||||
      1 MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNL 50

     51 TFTAQYLSYRIFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDW 100
      ||||||||||||||||||||||||||||||||||||||||||||||||
     51 TFTAQYLSYRIFQDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADEHSDW 100

    101 VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYN 150
      ||||||||||||||||||||||||||||||||||||||||||||||||
    101 VNITFCPVDDTIIGPPGMQVEVLADSLHMRFLAPKIENEYETWTMKNVYN 150

    151 SWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCVQVRGFLPDRNK 200
      ||||||||||||||||||||||||||||||||||||||||||||||||
    151 SWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCVQVRGFLPDRNK 200

    201 AGEWSEPVC EQTTHDVF GPSSS                                222
      ||||||||||||||||
    201 AGEWSEPVC EQTTHD.....                                215
```

IL10- R- β chain structure

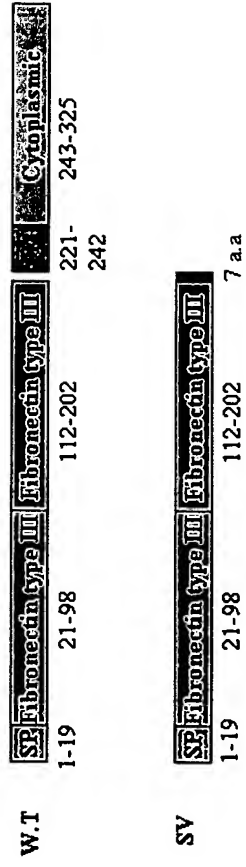


Fig. 32

Fig. 33a

INR1_T11 (SEQ ID NO: 43)

agaagaggcggtgctgtagagggcggtgagagctaagaggggcagcgctgtgcag
agggcggtgtgacttaggacggggcgatggcggtgagaggagctgcgcgtgcgcgaac
atgtaactgggtgggatctgcggcggtcccgatgATGgtcgtcctcctgggcgcgacga
ccctagtgtcgtcgccgtggcgccatgggtgttgtccgcagccgcaggtggaaaaaatc
taaaatctcctcaaaaagtagaggctcgacatcatagatgacaactttatcctgaggtgga
acaggagcgatgagtcgtcggaatgtgactttttcattcgattatcaaaaaactggga
tggaataattggataaaattgtctgggtgtcagaatattactagtaccaaagtcaactttt
cttcaactcaagctgaatgtttatgaagaaattaaattgctgtataagagcagaaaaagaaa
acacttcttcatggatgaggttgactcatttacaccatttcgcaaagctcagattggtc
ctccagaagtacatttagaagctgaagataaggcaatagtgtacacatctctcctggaa
caaaagatagtgttatgtgggctttggatgggttaagctttacatatagcttagttatct
ggaaaaactcttcaggtgtagaagaaaggattgaaaatatttattccagacataaaaattt
ataaaactctcaccagagactacttattgtctaaaagttaaagcagcactacttacgtcat
ggaaaattgggtgtctatagtcagtcattgtataaaagaccacagttgaaaatgaactac
ctccaccagaaaatatagaagtcagtggtccaaaatcagaactatgttcttaaatgggatt
atacatatgcaaactgacctttcaagttcagtggtccacgcctttttaaaaaggaatc
ctggaaaccatttgtataaatggaacaaatacctgactgtgaaaatgtcaaaactacc
agtgtgtctttcctcaaaacgtttttcaaaaaggaatttaccttctccgcgtacaagcat
ctgatggaaataacacatctttttgggtctgaagagataaagtttgatactgaaatacaag
cttctcacttctcctcagtcctttaacattagatcccttagtgattcattccatctctata
tcggtgtccaaaacagtcctggaaacacgcctgtgatccaggattatccactgatttatg
aaattattttttgggaaaacacttcaaagtctgagagaaaaattatcgagaaaaaaactg
atgttacagttcctaatttgaaccactgactgtatattgtgtgaaagccagagcacaca
ccatggatgaaaagctgaataaaaagcagtggttttttagtgacgctgtatgtgagaaaacaa
aaccaggtcagaatcttttattgtcttttttaaaaatgTACctagacataataaaaagtaa
ttctatactgta

Fig. 33b

INR1_T11 (SEQ ID NO: 41)

MVLLGATTLVLVAVAPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRWNRSDSVGNVTF
SFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVEEIKLRIRAEKENTSSWYEVDST
PFRKAQIGPPEVHLEAEDKAIVIHISPGTKDSVMWALDGLSFTYSLVIWKNSSGVEERIE
NIYSRHKIYKLSPETTYCLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQN
QNYVLKWDYTYANMTFQVQWLHAFLKRNPNGNHLKWKQIPDCENVKTTQCVFPQNVFQKG
IYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHIYIGAPKQSGNTPV
IQDYPLIYEIIFWENTSNAERKIIIEKKTDTVTPNLKPLTVYCVKARAHTMDEKLNKSSVF
SDAVCEKTKPGQNLLLSFLKM

FIGURE 34
Interferon- α/β -receptor-1-INR1

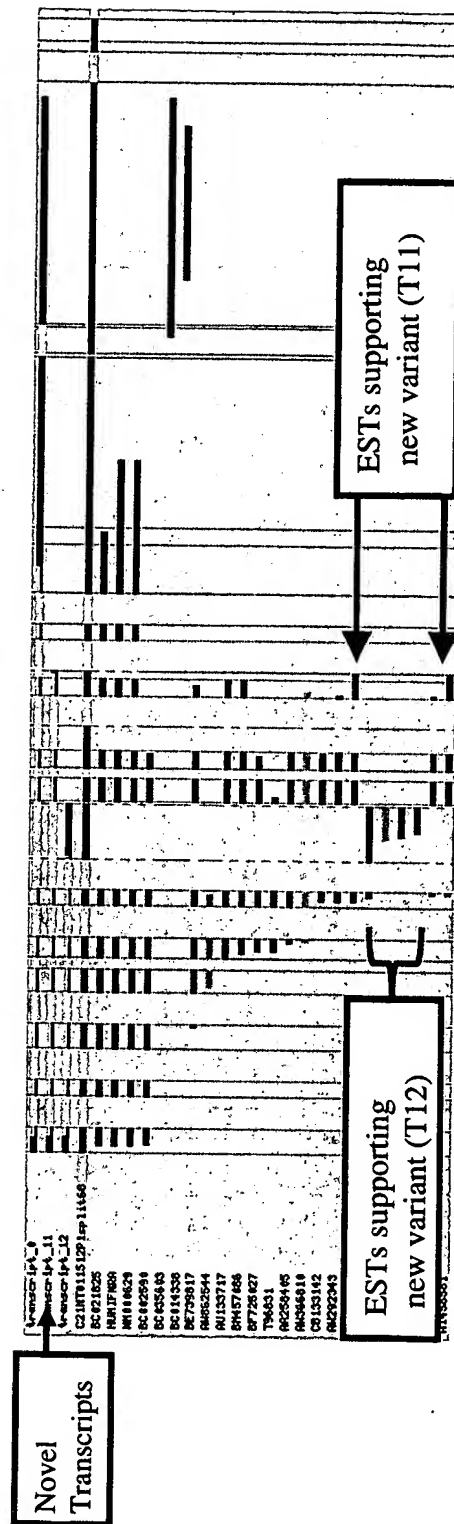


Fig. 35

t07758_p5(t11).pfs

Sequence name: /dir/tp/CGC/DATA/analysis_db/sw.fasta:INR1_HUMAN

Sequence documentation:

Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
Homo sapiens (Human). P17181;

Alignment of: T07758_P5 x INR1_HUMAN ..

```

1  MVVLLGATTLVLVAVAPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRW 48
   |||||
2  MVVLLGATTLVLVAVGPWVLSAAAGGKNLKSPQKVEVDIIDDNFILRW 49
   |||||
49  NRSDESVGNVTFSTFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVEE 98
   |||||
50  NRSDESVGNVTFSTFDYQKTGMDNWIKLSGCQNITSTKCNFSSLKLNVEE 99
   |||||
99  IKLRIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEAEDKAIVIHISPG 148
   |||||
100 IKLRIRAEKENTSSWYEVDSTPFRKAQIGPPEVHLEAEDKAIVIHISPG 149
   |||||
149 TKDSVMWALDGLSFTYSLVIWKNSSGVEERIEINIYSRHKIYKLSPETTY 197
   |||||
150 TKDSVMWALDGLSFTYSLLIWKNSSGVEERIEINIYSRHKIYKLSPETTY 198
   |||||
198 CLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKW 247
   |||||
199 CLKVKAALLTSWKIGVYSPVHCIKTTVENELPPPENIEVSVQNQNYVLKW 248
   |||||
248 DYTIANMTFQVQWLHAFKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVF 297
   |||||
249 DYTIANMTFQVQWLHAFKRNPGNHLYKWKQIPDCENVKTTQCVFPQNVF 298
   |||||
298 QKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHI 347
   |||||
299 QKGIYLLRVQASDGNNTSFWSEEIKFDTEIQAFLLPPVFNIRSLSDSFHI 348
   |||||
348 YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIEKKTDTVTPNLKP 397
   |||||
349 YIGAPKQSGNTPVIQDYPLIYEIIFWENTSNAERKIEKKTDTVTPNLKP 398
   |||||
398 LTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPGQNLLLSFLKM 441
   |||||
399 LTVYCVKARAHTMDEKLNKSSVFSDAVCEKTKPG..... 432
```

INR1 structure

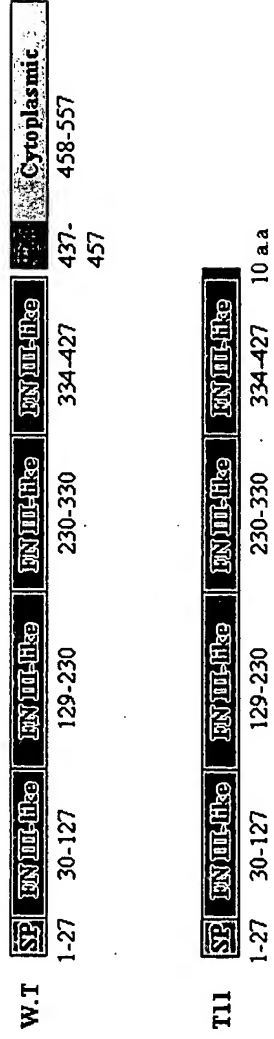


Fig. 36